

OM protein - protein search, using sw model	Run on: March 14, 2003, 04:41:21 ; (without alignments)	Search time 19.3258 Seconds
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Scoring table: BLOSSUM62	Sequence: 1 MKQILHPAELTTATMLFPVLL.....KHOIYRDSCAKASCNCNSIY 258	Scoring table: BLOSSUM62
Post-processing: Maximum Match 0%	Post-processing: Maximum Match 100%	Post-processing: Maximum Match 0%
Database : SwissProt_40:*	Database : SwissProt_40:*	Database : SwissProt_40:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
SUMMARIES		
Result No.	Score	Query Length
1	1363	94.9
2	988	68.9
3	968.5	67.4
4	929	64.7
5	830	57.8
6	766.5	53.4
7	755.5	52.6
8	671.5	46.8
9	617.5	43.0
10	552	38.4
11	529.5	36.9
12	328	22.8
13	274	19.1
14	269	18.7
15	265	18.5
16	259	18.0
17	257.5	17.9
18	254	17.7
19	252.5	17.6
20	251	17.5
21	250.5	17.4
22	250.5	17.4
23	250.5	17.4
24	248	17.3
25	245.5	17.1
26	243.5	17.0
27	243	16.9
28	241.5	16.8
29	240.5	16.7
30	238.5	15.9
31	227.5	15.8
32	222.5	15.5
33	222	15.5
ALIGNMENTS		
Result No.	Score	Query Length
1	1363	94.9
2	988	68.9
3	968.5	67.4
4	929	64.7
5	830	57.8
6	766.5	53.4
7	755.5	52.6
8	671.5	46.8
9	617.5	43.0
10	552	38.4
11	529.5	36.9
12	328	22.8
13	274	19.1
14	269	18.7
15	265	18.5
16	259	18.0
17	257.5	17.9
18	254	17.7
19	252.5	17.6
20	251	17.5
21	250.5	17.4
22	250.5	17.4
23	250.5	17.4
24	248	17.3
25	245.5	17.1
26	243.5	17.0
27	243	16.9
28	241.5	16.8
29	240.5	16.7
30	238.5	15.9
31	227.5	15.8
32	222.5	15.5
33	222	15.5
RESULT 1		
CRS3_HUMAN	CRS3_HUMAN	STANDARD:
ID	P54108	PRT: 245 AA.
AC	015512;	
DT	01-OCT-1996 (Rel. 34, Created)	
DT	01-OCT-1996 (Rel. 34, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Cysteine-rich secretory protein-3 precursor (CRISP-3) (SGP28 protein).	
GN	CRISP3.	
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI_TaxID	9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=95186934; PubMed=8601434;	
RA	Kjelleosen J.B., Borregaard N.;	
RA	"SGP28, a novel matrix glycoprotein in specific granules of human neutrophils with similarity to a human testis-specific gene product neutrophils and a related sperm-coating glycoprotein.",	
RT	FEBS Lett. 380:246-250(1996).	
RT	- SUBCELLULAR LOCATION: SECRETED; IN NEUTROPHILS, LOCALIZED IN SPECIFIC GRANULES	
CC	- TISSUE SPECIFICITY: SALIVARY GLAND, PANCREAS AND PROSTATE > EPIIDIDYMIS, OVARY, THYMUS AND COLON.	
CC	- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.	
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EMBL	X95440; CAA64527.1; -.	
EMBL	X94333; CAA63984.1; -.	
HSSP	P35778 solenopsis	
DR	Interpro: IPR001283; Allrgn_V5/Tpx1.	
DR	Pfam: PF00188; SCP_1.	
PRINTS	PRO0837; V5TP1LIKE.	
DR	PRODOM: PDO00542; Allrgn_V5/Tpx1; 1.	
DR	SMART: SMD019; SCP_1.	
DR	PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.	
DR	PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.	
KW	glycoprotein; signal; multigene family; polymorphism; SIGNAL	

RA Kasahara M., Gutknecht J., Brew K., Spurr N., Goodfellow P.N.;
 RT "Cloning and mapping of a testis-specific gene with sequence
 RT similarity to a sperm-coating glycoprotein gene.";
 RL Genomics 5:527-534(1989).

CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- TISSUE SPECIFICITY: TESTIS.
 CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
 CC INSECTS AG3/AG5; FUNGI SC1/SC14 AND PLANTS PR-1.

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CC EMBL; M25533; AAA0472.1; -.
 DR PIR; A33329.
 DR HSSP; P04284; ICFP.
 DR MGI; 98815; TPX1.
 DR InterPro; IPR001283; Allrgn_v5/TPx1.
 DR Pfam; PF00188; SCP; 1.
 DR PRINTS; PRO0037; V5PXLKE.
 DR PRODOM; P000542; Allrgn_v5/TPx1; 1.
 DR SMART; SM00198; SCP; 1.
 DR PROSITE; PS01009; SCP_AGS5_PRL_SC7_1; 1.
 DR PROSITE; PS01010; SCP_AGS5_PRL_SC7_2; 1.
 DR KW Testis; Signal; 1; 22
 FT SIGNAL; 1; 22
 FT CHAIN; 23; 243
 FT SEQUENCE; 243 AA; 27605 MW; 6E7F59ACAA244 CRC64;
 SQ Query Match, 57.8%; Score 830; DB 1; Length 243;
 Best Local Similarity 59.6%; Pred. No. 6.8e-64; Mismatches 58; Indels 2; Gaps 2;
 Matches 146; Conservative 39; Sequence 243 AA; 27605 MW; 6E7F59ACAA244 CRC64;
 Oy 14 MTLFPLFLVAGLULPSFPRANEDKPAFFTALLTPTQVOREIVVKHNEERRAVSPARNM 73
 Db 1 MAWFOVMLFVFLLRLRS-PLTEGKOPDFPSLTLNQLQVERIVVKHNEERRAVSPARNM 59
 Oy 74 LKMEWKKEAAANQKWAQNCNRYHSNPKORMTSKCGEYLMMSSAPSSHSQATOSWFDEY 133
 Db 60 LKMEWQIQTNTAQKWAQNCNRYHSNPKORMTSKCGEYLMMSSAPSSHSQATOSWFDEY 119
 Oy 134 NDFDFGVGKTPNAVQHTQVWVWSSYLVGGNAYCPCNPKVVKLYYYQYCPCAGNWNR 193
 Db 120 EDFVYGVGK-PNSAVGHTQVWVWSSYLVGGNAYCPCNPKVVKLYYYQYCPCAGNWNR 178
 Oy 194 LYVPEQGARPCASCNDCDCGCTNGCKEDYLNCSKSLKLTLCKHOLVRDCKASNC 253
 Db 179 KSTPQOOGPCASCNDCDCGCTNGCKEDYLNCSKSLKLTLCKHOLVRDCKASNC 238
 Oy 254 SNSVY 258
 Db 239 EDKIH 243

RESULT 6

AEG1_MOUSE STANDARD PRT; 244 AA.

AC 003401; 01-OCT-1993 (Rel. 27, Created)
 AC 01-OCT-1993 (Rel. 27, last sequence update)
 AC 15-JUN-2002 (Rel. 41, last annotation update)
 DE Sperm-coating glycoprotein 1 precursor (SCP 1) (Acidic epididymal
 DE glycoprotein 1) (Cysteine-rich secretory protein-1) (Crisp-1).
 DE AEG1 OR AEG-1.
 OS Mus musculus (Mouse).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090; 1]

RP SEQUENCE FROM N.A.
 RC TISSUE-Submandibular gland;
 RX MEDLINE-93246016; PubMed-1301383;
 RA Mizuki N., Kasahara M.;
 RL "Mouse submandibular glands express an androgen-regulated transcript
 RT encoding an acidic epididymal glycoprotein-like molecule.";
 RL Mol. Cell. Endocrinol. 89:25-32(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Submandibular gland;
 RX MEDLINE-93307144; PubMed-8319566;
 RA Haendler B., Kratzschmar J., Theuring F., Schleuning W.D.;
 RT "Transcripts for cysteine-rich secretory protein-1 (CRISP-1; DE/AEG)
 RT and the novel related CRISP-3 are expressed under androgen control in
 RT the mouse salivary gland.";
 RL Endocrinology 133:192-198(1993).
 CC -!- FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOA UNDERGO
 CC FUNCTIONAL MATURATION WHILE THEY MOVE FROM THE TESTIS TO THE
 CC DUCTUS DEFERENS.
 CC -!- SUBCELLULAR LOCATION: STORED IN SECRETORY GRANULES OF GRANULAR
 CC CONVOLUTED TUBULE CELLS.
 CC -!- TISSUE SPECIFICITY: MAINLY FOUND IN THE CAUDA EPIDIDYMIS WHERE IT
 CC IS SYNTHESIZED BY THE PRINCIPAL CELLS AND SECRETED INTO THE LUMEN.
 CC BINDS TO THE HEADS OF SPERMATOZOA. ALSO EXPRESSED IN THE
 CC SUBMANDIBULAR GLAND.
 CC -!- DEVELOPMENTAL STAGE: EXPONENTIAL INCREASE BETWEEN DAYS 25 AND 30
 CC AFTER BIRTH.
 CC -!- INDUCTION: By androgens.
 CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
 CC INSECTS AG3/AG5; FUNGI SC1/SC14 AND PLANTS PR-1.

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CC EMBL; M92849; AAA37460.1; -.
 DR PIR; A49202; A49202.
 DR MGI; 102553; Aeg1.
 DR InterPro; IPR001283; Allrgn_v5/TPx1.
 DR Pfam; PF00188; SCP; 1.
 DR PRINTS; PRO0037; V5PXLKE.
 DR PRODOM; P000542; Allrgn_v5/TPx1; 1.
 DR SMART; SM00198; SCP; 1.
 DR PROSITE; PS01010; SCP_AGS5_PRL_SC7_1; 1.
 DR KW Sperm; Glycoprotein; Signal.
 DR FT SIGNAL; 1; 19
 FT CHAIN; 20; 244
 FT CARBOHYD; 145; 145
 FT SEQUENCE; 244 AA; 27679 MW; D0DD0348F85781F CRC64;
 SQ Query Match, 53.4%; Score 766.5; DB 1; Length 244;
 Best Local Similarity 55.1%; Pred. No. 1.8e-58; Mismatches 70; Indels 1; Gaps 1;
 Matches 135; Conservative 39; Sequence 244 AA; 27679 MW; D0DD0348F85781F CRC64;
 Oy 14 MTLFPLFLVAGLULPSFPRANEDKPAFFTALLTPTQVOREIVVKHNEERRAVSPARNM 73
 Db 1 MALMLVFLFLAVLIPPLPSLQDSSQENRERLKLSTTRMSVQEELVKHNLRRMSPSGDL 60
 Oy 74 LKMEWKKEAAANQKWAQNCNRYHSNPKORMTSKCGEYLMMSSAPSSHSQATOSWFDEY 133
 Db 61 LKMEWQIQTNTAQKWAQNCNRYHSNPKORMTSKCGEYLMMSSAPSSHSQATOSWFDEY 120
 Oy 134 NDFDFGVGKTPNAVQHTQVWVWSSYLVGGNAYCPCNPKVVKLYYYQYCPCAGNWNR 193
 Db 121 KDLTYDVGKQPDWSVQHTQVWVWSSYLVGGNAYCPCNPKVVKLYYYQYCPCAGNWNR 179
 Oy 194 LYVPEQGARPCASCNDCDCGCTNGCKEDYLNCSKSLKLTLCKHOLVRDCKASNC 253

Db	180	LYTPVTAGERCASCPCPDHCEGCTNSCGHDKVYKVKLMSCEHLLKKGGKATCLC	239	FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL). FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL). FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
Oy	254	SNSIY	258	SO SEQUENCE 246 AA; 27847 MW; 585207C/CFTCF9D1 CRC64;
Db	240	EGKIH	244	Query Match 52.6%; Score 755.5; DB 1; Length 246; Best Local Similarity 55.1%; Pred. No. 1.6e-57; Matches 136; Conservative 35; Mismatches 73; Index 3; Gaps 2;
RESULT 7				
AEG_RAT				
ID AEG_RAT		STANDARD;	PRT;	246 AA.
AC P12020;				
DT 01-OCT-1989 (Rel. 12, Last sequence update)				
DT 15-JUN-2002 (Rel. 41, Last annotation update)				
DE Sperm-coating glycoprotein precursor (SCP) (Acidic epididymal glycoprotein) (Protein D) (Protein E) (Protein IV) (Sialoprotein) (32 kDa epididymal protein).				
DE Rattus norvegicus (Rat).				
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX NCBI_Taxid=10116;				
RN 14				
RP MTLEPVFLFLIVAGLURSF--PANEKDPAFTALLTITQTOVQRETYVNHNLRRAYSPPAR 71				
RC 1				
RT MALMLVLLFLAVLVPPLSLQDTTDEWDRLKENLSTTKSYQEETINKHNLRLRTVSPSGS 60				
Qy 72				
DB NMLKQEWNKERAAANQKWAQNCQNYHNSPKDRMTSLSKCGNLYMSAPPSSQATQSWFD 131				
Qy 61				
DB DLRYEVWDHDAYVNQKWAQNCQYHNSPKDRMTSLSKCGNLYMSAPPSSQATQSWFD 120				
Qy 132				
DB EYNDDFGVGKPTPAVWGHYQTVWYSSIVLVCQGNAYCPNQKVUKYYCQYCPAGNWA 191				
DB 121				
DB ESLDVFVGFPCPKKVQKVGHYQTVWNTFLVACQVAECPDQ-LKYFVYCHQPGNTV 179				
Qy 192				
DB NRLYSPTEGEGPCDSCPGNCEDGLCTNSCBEYDNYNSNCGLKKMVSDDPLKEGCRASC 251				
DB 180				
GRLYSPTEGEGPCDSCPGNCEDGLCTNSCBEYDNYNSNCGLKKMVSDDPLKEGCRASC 239				
Qy 252				
DB NCSNSTY 258				
Db 240				
FCEDKIH 246				
RESULT 8				
RP HELO_HELHO				
ID HELO_HELHO		STANDARD;	PRT;	242 AA.
AC 091055;				
DT 01-NOV-1997 (Rel. 35, Created)				
DT 01-NOV-1997 (Rel. 35, Last sequence update)				
DT 15-JUN-2002 (Rel. 41, Last annotation update)				
DE Helothermine precursor (HlTx).				
OS Heloderma horridum horridum (Mexican beaded lizard).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Helodermatidae; Heloderma.				
OC NCBITaxid=8552;				
RN 11				
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.				
RC TISSUE=Salivary gland;				
RX MEDLINE=93375162; PubMed=7647234;				
RA Morrisette J., Kraetschmar J., Haendler B., El-Hayek R.,				
RA Mochica-Morales J., Martin B.M., Patel J.R., Moss R.L.,				
RA Schleuning W.-D., Coronado L.D., Possani L.D.,				
CC "Primary structure and properties of helothermine, a peptide toxin that blocks ryanodine receptors.,"				
CC Rb. 68:2280-2288(1995).				
CC RP SEQUENCE OF 20-39, AND CHARACTERIZATION.				
CC TISSUE=Venom;				
RX MEDLINE=90260878; PubMed=1693019;				
RA Mochica Morales J., Martin B.M., Possani L.D.,				
RT "Isolation and characterization of helothermine, a novel toxin from Heloderma horridum horridum (Mexican beaded lizard) venom.,"				
RT Toxicon 28:29-30(1990).				
CC -i- FUNCTION: Toxin that blocks ryanodine receptors. It is toxic to mice; it causes lethargy, partial paralysis of rear limbs and lowering of body temperature.				
CC -i- SUBCELLULAR LOCATION: Secreted.				
CC -i- TISSUE SPECIFICITY: Produced by the venomous gland.				
CC -i- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC1/SC14 AND PLANTS PR-1.				
CC				
RESULT 9				
RP SIGNAL_1				
FT CHAIN_20				
FT MOD_RES_20				
FT CARBOHYD_32				
CC SPERM-COATING GLYCOPROTEIN.				
CC BLOCKED (POTENTIAL).				
CC N-LINKED (GLCNAC. . .) (POTENTIAL).				
CC				

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CC EMBL: U13619; AAC59730.1; -

CC DR InterPro: IPR001283; Allrgn_V5/Tpx1.

CC DR Pfam: PF0018; SCP_1.

CC DR PRINTS: PR00837; V5TPX1LIKE.

CC DR Prodom: PD000542; Allrgn_V5/Tpx1; 1.

CC DR SMART: SM0198; SCP_1.

CC DR PROSITE: PS01009; SCP_AGS_PRL_SC7_2; FALSE_NEG.

CC KW Calcium channel inhibitor; Neurotoxin; Toxin; Signal.

CC FT SIGNAL 1 19

CC FT CHAIN 20 242 HELOTHERMINE.

CC SEQUENCE 242 AA; 27493 MW; 0E183F22925DF3 CRC64;

Query Match 46 8%; Score 671 5; DB 1; Length 242; Best Local Similarity 50 2%; Pred. No. 2.3e-50; Matches 123; Conservative 31; Mismatches 86; Indels 5; Gaps 3;

Qy 14 MTLPVLLFLVAGLIPSPFANEDKPAFFALLTQTOVOREINKHNERPRAVSPARM 73

Db 1 MILLSLYLGGLAAMHQS--EGEASPKLGLMMNSPDQOTEITDKHNNRURTEPTASM 57

Qy 74 LKMEWNEKAANQKWAQNCNYRHNSNPDR-WMSLKCGENLYMSSAPSSWQATOSWDFE 132

Db 58 LKMEWNEKAANQKWAQNCNYRHNSNPDR-WMSLKCGENLYMSSAPSSWQATOSWDFE 117

Qy 133 YNDFDPFGVQPKTPNVAUGHQHTQVWVWYSSILVGGGNAYPNOKVILKYYVQCYPAGNNAN 192

Db 118 RKYIFRFNIGPTAQNMIGHTQVWVWYRSYELGKAIAYCPDQPTVQYQVQCYCPGNNIRS 177

Qy 193 RLVYIPEGARCAASCPCDNGGCTGNGKEDLYSNCSSLKLTICKHOLVRASKAN 252

Db 178 RKYIFRFNIGPTAQNMIGHTQVWVWYRSYELGKAIAYCPDQPTVQYQVQCYCPGNNIRS 236

Qy 253 CSNS1 257

Db 237 CLUTER 241

RESULT 9

AEG2_MOUSE STANDARD; PRT; 241 AA.

ID 001402; DT 01-OCT-1993 (Rel. 27, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

DE Sperm-coating glycoprotein 2 precursor (SCP 2) (Acidic epididymal glycoprotein 2) (Cysteine-rich secretory protein-3) (Crisp-3).

GN AEG2 OR AEG-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBL_TaxID=10090;

RN [1]

SEQUENCE FROM N.A.

RC TISSUE-Submandibular gland; MEDLINE=93246016; PubMed=1301383;

RT "Mouse submandibular glands express an androgen-regulated transcript encoding an acidic epididymal glycoprotein-like molecule.";

RL Mol. Cell. Endocrinol. 89:29-32(1992).

RN [2]

SEQUENCE FROM N.A.

RC TISSUE-Submandibular gland; MEDLINE=9307144; PubMed=8319566;

RA Haendler B., Kratzschmar J., Theuring F., Schleuning W.D.;

RT "Transcripts for cysteine-rich secretory protein-1 (CRISP-1; DE/AEG) and the novel related CRISP-3 are expressed under androgen control in the mouse salivary gland.";

RL Endocrinology 133:192-198(1993).

RESULT 10

CRPV_TRIMU STANDARD; PRT; 183 AA.

ID CRPV_TRIMU

AC P79845;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Cysteine-rich venom protein precursor (CRPV).

OS Trimeresurus mucrosquamatus (Taiwan habu).

CC -!- FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOA UNDERGO DUCTUS DEFERENS.

CC CC -!- SUBCELLULAR LOCATION: STORED IN SECRETORY GRANULES OF GRANULAR TISSUE SPECIFICITY: EXPRESSED IN SUBMANDIBULAR GLAND.

CC CC -!- DEVELOPMENTAL STAGE: EXPONENTIAL INCREASE BETWEEN DAYS 25 AND 30 AFTER BIRTH.

CC CC -!- INDUCTION: By androgens.

CC CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/Tpx1; INSECTS AG3/AG5; FUNGI SCP/SC14 AND PLANTS PR-1.

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CC DR EMBL: M92850; AAA37186.1; -

CC DR EMBL: L05560; AAA37461.1; -

CC DR PIR: B49202; B49202.

CC DR MGD: MGI-102552; Aeg2.

CC DR InterPro: IPR001283; Allrgn_V5/Tpx1.

CC DR Pfam: PF00188; SCP_1.

CC DR PRINTS: PR00837; V5TPX1LIKE.

CC DR Prodom: PD000542; Allrgn_V5/Tpx1; 1.

CC DR SMART: SM0198; SCP_1.

CC DR PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.

CC DR PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.

CC KW SIGNAL 1 19

CC FT CHAIN 20 241 SPERM-COATING GLYCOPROTEIN 2.

CC FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC SEQUENCE 241 AA; 27314 MW; D903788B4E4001EF CRC64;

Query Match 43 8%; Score 617 5; DB 1; Length 241; Best Local Similarity 48 4%; Pred. No. 9.1e-46; Matches 118; Conservative 40; Mismatches 79; Indels 7; Gaps 3;

DR	EMBL: U16307; AAA82731; 1;	DR	HSSP: P04284; 1CE.
DR	MIN: 602692; -;	DR	MINP: 602692; -;
DR	INTERPRO: IPR0012833; Allrgn_V5/Tpx1.	DR	INTERPRO: IPR0012833; Allrgn_V5/Tpx1.
DR	PRINTS: PRO0108; SCP; 1.	DR	PRINTS: PRO0108; SCP; 1.
DR	PRODOM: PD00542; Allrgn_V5/Tpx1; 1.	DR	PRODOM: PD00542; Allrgn_V5/Tpx1; 1.
DR	SMART: SMD0198; SCP; 1.	DR	SMART: SMD0198; SCP; 1.
DR	PROSITE: PS01010; SCP_AG5_PRL_SC7_1; 1.	DR	PROSITE: PS01010; SCP_AG5_PRL_SC7_1; 1.
FT	CONFFLICT 125 125 D->N (IN REF. 2).	FT	CONFFLICT 125 125 D->N (IN REF. 2).
FT	RQDQVKYRQSVVPGWPMRNYRTSLFLIVNSVILILSYT (IN REF. 2).	FT	RQDQVKYRQSVVPGWPMRNYRTSLFLIVNSVILILSYT (IN REF. 2).
FT	LITLWQKPVNLLD->DSTPKSNVTTMIVYRIRHIS	FT	LITLWQKPVNLLD->DSTPKSNVTTMIVYRIRHIS
SQ	SEQUENCE 266 AA: 30342 MN: C04378085EFB2B7A CRC64;	SQ	SEQUENCE 266 AA: 30342 MN: C04378085EFB2B7A CRC64;
QY	Query Match 9 22.8%; Score 328; DB 1; Length 266;	QY	Query Match 9 22.8%; Score 328; DB 1; Length 266;
QY	Best Local Similarity 34.9%; Pred. No. 5.2e-21; Mismatches 71; Indels 46; Gaps 12;	QY	Best Local Similarity 34.9%; Pred. No. 5.2e-21; Mismatches 71; Indels 46; Gaps 12;
QY	Matches 81; Conservatve 34; ASP_ANCCA 100;	QY	Matches 81; Conservatve 34; ASP_ANCCA 100;
DB	1 MRVTLATIAWMMVSFVNNSHTANILPDT-ENED------FIKDCVRTHNKKFR 45	DB	1 MRVTLATIAWMMVSFVNNSHTANILPDT-ENED------FIKDCVRTHNKKFR 45
QY	64 RAVSPPRNMLMEFNEAAANQKWAQCNVYHS--NPKDM---TSIKGENYMS 116	QY	64 RAVSPPRNMLMEFNEAAANQKWAQCNVYHS--NPKDM---TSIKGENYMS 116
DB	46 SEVQPTASDMLYMTWDPLA0IAKAWASNC0FSHNTRLKPPHKLHNPFTSL--GENTWIG 103	DB	46 SEVQPTASDMLYMTWDPLA0IAKAWASNC0FSHNTRLKPPHKLHNPFTSL--GENTWIG 103
QY	117 SAP-SSNSQAIQSWFDEYNDFFGFGVKPKTPNAVGHVTQVMWSSYLVCGNAYCPNOKV 175	QY	117 SAP-SSNSQAIQSWFDEYNDFFGFGVKPKTPNAVGHVTQVMWSSYLVCGNAYCPNOKV 175
DB	104 SVPFIVSSAIIQNWDEQDQDPIKT--RICKYQHHTQYVWRSYDVKYGCANQFCP--KV 159	DB	104 SVPFIVSSAIIQNWDEQDQDPIKT--RICKYQHHTQYVWRSYDVKYGCANQFCP--KV 159
QY	176 LKY-----YVVOQCPAGNNWANRLYVPPYEOGAPCASCPCDN--CDDGICTN 218	QY	176 LKY-----YVVOQCPAGNNWANRLYVPPYEOGAPCASCPCDN--CDDGICTN 218
DB	160 SGFDALSNGAHFICNYGGNNIPT--WPKYKRGATCSACPNNDKCLDNLCVN 208	DB	160 SGFDALSNGAHFICNYGGNNIPT--WPKYKRGATCSACPNNDKCLDNLCVN 208
QY	RESULT 13	QY	RESULT 13
ID	ASP_ANCCA STANDARD; PRT; 424 AA.	ID	ASP_ANCCA STANDARD; PRT; 424 AA.
AC	Q16937; 1	AC	Q16937; 1
DT	01-NOV-1997 (Rel. 35, Created)	DT	01-NOV-1997 (Rel. 35, Created)
DT	30-MAY-2000 (Rel. 39, Last annotation update)	DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	Ancylostoma secreted protein precursor	DE	Ancylostoma secreted protein precursor
GN	ASP.	GN	ASP.
OS	Ancylostoma caninum (Dog hookworm).	OS	Ancylostoma caninum (Dog hookworm).
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.	OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
OX	NCBI_TAXID=29170;	OX	NCBI_TAXID=29170;
RN	STRUCTURE BY NMR.	RN	STRUCTURE BY NMR.
RX	MEDLINE:98151500; PubMed=9482873;	RX	MEDLINE:98151500; PubMed=9482873;
RA	Szeverstki T., Fernandez C., Mumenthaler C., Wuethrich K.;	RA	Szeverstki T., Fernandez C., Mumenthaler C., Wuethrich K.;
RT	"Structure comparison of human glioma pathogenesis-related protein p14a indicates a functional link between the human immune system and a plant defense system."	RT	"Structure comparison of human glioma pathogenesis-related protein p14a indicates a functional link between the human immune system and a plant defense system."
RT	Proc. Natl. Acad. Sci. U.S.A. 95:2262-2266(1998).	RT	Proc. Natl. Acad. Sci. U.S.A. 95:2262-2266(1998).
CC	-- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE HUMAN BRAIN TUMOR, BUT NEITHER IN NORMAL FETAL GLIOBLASTOMA MULTIFORM/ASTROCTOMA, NOR IN OTHER NERVOUS SYSTEM TUMORS.	CC	-- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE HUMAN BRAIN TUMOR, BUT NEITHER IN NORMAL FETAL GLIOBLASTOMA MULTIFORM/ASTROCTOMA, NOR IN OTHER NERVOUS SYSTEM TUMORS.
CC	-- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/Tpx1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.	CC	-- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/Tpx1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC	-----	CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----	CC	-----
DR	EMBL: U26187; AAC47001; 1; -.	DR	EMBL: U26187; AAC47001; 1; -.
DR	HSSP: P04284; 1CE.	DR	HSSP: P04284; 1CE.

DR InterPro: IPR001283; Allrgn_V5/Tpx1.
 DR Pfam: PF00188; SCP; 1.
 DR PRINTS; PR00837; V5TPX1LIKE.
 DR PRODOM: PD000542; Allrgn_V5/Tpx1; 2.
 DR SMART; SM00198; SCP; 2.
 DR PROSITE; PS01009; SCP_AGS_PRL_SC7_1; FALSE_NEG.
 DR PROSITE; PS01010; SCP_AGS_PRL_SC7_2; FALSE_NEG.
 KW Signal.

FT CHAIN 1 18 POTENTIAL.
 SEQUENCE 424 AA; 45735 MW; 4B8295P5D3015F9 CRC64;

Query Match 19.1%; Score 274; DB 1; Length 424;
 Best Local Similarity 31.1%; Pred. No. 3..5e-16; Mismatches 70; Indels 44; Gaps 9; Matches 68; Conservative 37; Mismatches 70; Indels 44; Gaps 9;

QY 29 PSFPANEDKDPAPFTALLTTOVOREIVNKHNLRRAV-----SPPARNMLKM 76
 DB 218 PDVPETNQOCPSNTGKTDs---VRDTFLSVHNEFRSSVARGLEPDALGGNAPKAQMLKM 274

QY 77 EWKNERAAQNAQKWAQNCNYKHSNPDRMTSLKCGENLYMSSA-----PSSWSQATQSWEQ 131
 DB 275 VDCEVEASAIRHNGKNCVQHSGEDPR---GLGENIYKNSVLFDKNKRAKQNSOLWNN 331

QY 132 EYNDDFGVPKTT-----PNAVGHTQVWVNSYLVCGNAYCPNOKVLYKYYVC 182
 DB 332 BLK- EFGVGPSPNVLTTALNRRGKQHGTQMANDTYKLGCAVFCNDF---FGVC 385

QY 183 QYCPAGNWNARLVLVYVEQGAPCASCQPD---NCDDPGIQT 217
 DB 386 QYGGPGNYMG--HVIYTMGQPCSCSPGATCSVTEGLCS 422

RESULT 14

VA51_VESCR STANDARD; PRT; 202 AA.
 ID VA51_VESCR STANDARD; PRT; 202 AA.
 AC P35781;
 DT 01-JUN-1994 (Rel. 29; Created)
 DT 01-JUN-1994 (Rel. 29; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE venom allergen 5.01 (Antigen 5-1) (AG5-1) (Allergen vesp c 5.01) (vesp c V.01).
 OS Vespa crabro (European hornet).
 OC Insecta; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Aculeata; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
 OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
 OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
 RN [1]
 RN NCBI_TaxID=7445;
 RP SEQUENCE.

VA52_VESCR STANDARD; PRT; 202 AA.
 ID VA52_VESCR STANDARD; PRT; 202 AA.
 AC P35782;
 DT 01-JUN-1994 (Rel. 29; Created)
 DT 01-JUN-1994 (Rel. 29; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE venom allergen 5.02 (Antigen 5-2) (AG5-2) (Allergen vesp c 5.02) (vesp c V.02).
 OS Vespa crabro (European hornet).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
 OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
 OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
 RN [1]
 RP SEQUENCE.

TISSUE="Venom";
 RX MEDLINE=9444316; PubMed=8227862;
 RA Hoffmann D.R.;
 RT "Allergens in Hymenoptera venom. XXV: The amino acid sequences of antigen 5 molecules and the structural basis of antigenic cross-reactivity";
 RL J. Allergy Clin. Immunol. 92:707-716(1993).
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
 DR PIR: H44522; H44522.
 DR HSSP; P04284; 1CFE.
 DR InterPro: IPR001283; Allrgn_V5/Tpx1.
 DR Pfam: PF00188; SCP; 1.
 DR PRINTS; PR00837; V5TPX1LIKE.
 DR PRODOM: PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART; SM00198; SCP; 1.
 DR PROSITE; PS01009; SCP_AGS_PRL_SC7_1; 1.
 DR PROSITE; PS01010; SCP_AGS_PRL_SC7_2; 1.
 KW Venom; Allergen.

FT DISULFID 4 16 BY SIMILARITY.
 FT DISULFID 8 101 BY SIMILARITY.
 FT DISULFID 26 94 BY SIMILARITY.
 FT DISULFID 168 185 BY SIMILARITY.

FT DISULFID 16 BY SIMILARITY.
 FT DISULFID 8 101 BY SIMILARITY.
 FT DISULFID 26 94 BY SIMILARITY.
 FT DISULFID 168 185 BY SIMILARITY.

Query Match 18.5%; Score 265; DB 1; Length 202;
 Best Local Similarity 36.6%; Pred. No. 9..1e-16; Mismatches 60; Indels 20; Gaps 5;

QY 45 LTTOQVOREIVNKHNLRRAV-----PPARNLKMTWNKRAANQKWAQ 92
 DB 36 LTKOENL-EILKQHNEFRKVGARGLETRGNPGPQPKSMNTLVNDELAQIAQWNAQ 93

QY 93 CNYRHSNPKDRMTSLKCGENLYMSSA---SWSQAIOSWFDEINDFPFGVGKPTPNAV 148
 DB 94 CNYGDNCRN-SAKYSVGQNAIAGSTTADONPGSVSNKMKWDEDEVKDYQG-SPRNKLK 151

Oy	149	VGHYTOVWYSSVLVGGCNAYCPNQKVLYKKYYCQYCPAGNWAN	192
Db	152	VGHYTOVWYSSVLVGGCNAYCPNQKVLYKKYYCQYCPAGNWAN	195

Search completed: March 14, 2003, 05:40:55
Job time : 21.3258 secs

Job time : 21.3258 secs